P-264 - DEVELOPING AN AFFORDABLE BUT RELIABLE HUMAN BLOOD EX VIVO MODEL TO ANALYSE GENE EXPRESSION BY STAPHYLOCOCCUS EPIDERIMIDIS

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Background

Staphylococcus epidermidis is a commensal inhabitant of healthy human skin and mucosae. However, when external barriers, such as the skin, are damaged, the bacterium gains accesses into the bloodstream and emerges as an opportunistic pathogen. *S. epidermidis* can originate important infections such as medical device-associated bloodstream infections. This is mainly due to its ability to attach and form biofilms on the surface of vascular catheters. Hence, due to the clinical relevance of *S. epidermidis* medical device-associated bloodstream infections, human blood is frequently used as an *ex vivo* model, to mimic the environment encountered by the bacterium and study its behavior. An important limitation in the use of human blood is the availability of donors and the considerable quantity of blood necessary. As any other biological resource, the use of blood shall be reduced to a minimum and, thus, our goal was to test the influence of different volumes of human blood on the stability of *S. epidermidis* gene expression and on bacterial culturability.

Method

For this study, planktonic cells of *S. epidermidis* PT12003 (isolated from a patient after a stomach surgery) and SECOM005A (isolated from healthy human skin) were used. Different volumes of human blood (600, 500 and 200 µl) were tested using a multiplicity of infection of 1 neutrophil to 100 bacteria, and compared with the results obtained with a previously optimized *ex vivo* model (1 mL of blood, França et al., 2016). After 2 hours of incubation at 37ºC and slight agitation, the transcription levels of three genes was determined using quantitative PCR (qPCR). The number of culturable bacteria was determined by CFU counting.

Results & Conclusions

The results demonstrated that smaller volumes of human blood (up to 200 µl) did not significantly affect the transcription levels of the studied genes nor the culturability of bacterial cells, suggesting that lower quantity of blood can be used in *ex vivo* studies addressing gene expression studies. Furthermore, specific differences found between isolates were constant in all volumes.

References & Acknowledgments

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